

sequence encoding a polypeptide having fumonisin esterase activity and a sequence encoding a polypeptide having amine oxidase activity; and,

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b) stably integrating into the genome of said plant cell a secondary nucleotide sequence operably linked to a second promoter active in said plant cell, wherein said secondary nucleotide sequence has at least 90% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, wherein said sequence encodes a polypeptide having fumonisin detoxification activity.

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3. The method of claim 1, wherein said primary nucleotide sequence encoding a polypeptide having amine oxidase activity is an amino polyolamine oxidase.

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8. The method of claim 1, wherein at least one of said first promoter and said second promoter is an inducible promoter.

9. The method of claim 8 further comprising inducing expression of said primary and said secondary nucleotide sequences for a time sufficient to reduce pathogenicity of said fungus.

10. A plant having stably integrating into its genome

a) a primary nucleotide sequence operably linked to a promoter active in said plant, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,

b) a secondary nucleotide sequence operably linked to a promoter active in said plant, wherein said secondary nucleotide sequence has at least 90% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, wherein said sequence encodes a polypeptide having fumonisin detoxification activity.

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12. The plant of claim 10, wherein said primary nucleotide sequence encoding a polypeptide having amine oxidase activity is an amino polyolamine oxidase.

13. The plant of claim 10, wherein the primary nucleotide sequence stably incorporated into the plant cell comprises a sequence encoding a polypeptide having fumonisin esterase activity and a sequence encoding a polypeptide having amino oxidase activity.

17. Transformed seed of the plant of claim 10.

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18. A plant cell having stably integrating into its genome

- a primary nucleotide sequence operably linked to a promoter active in said plant cell, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,
- a secondary nucleotide sequence operably linked to a promoter active in said plant, wherein said secondary nucleotide sequence has at least 90% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, wherein said sequence encodes a polypeptide having fumonisin detoxification activity.

19. A method of reducing pathogenicity of a fungus that produces fumonisin, comprising stably integrating into the genome of a plant cell:

- a primary nucleotide sequence operably linked to a promoter active in said plant cell, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,
- a secondary nucleotide sequence operably linked to a promoter active in said plant cell, wherein said secondary nucleotide sequence comprises at least one sequence selected from the group consisting of a nucleotide sequence set forth in one of SEQ ID NO: 2, 4,

7, and 10.

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20. A plant having stably integrating into its genome

- a primary nucleotide sequence operably linked to a promoter active in said plant cell, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,
- b) a secondary nucleotide sequence operably linked to a promoter active in said plant, wherein said secondary nucleotide sequence comprises at least one sequence selected from the group consisting of a nucleotide sequence set forth in one of SEQ ID NO: 2, 4, 7, and 10.

Please add the following new claims:

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21. The method of claim 1, wherein said secondary nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

22. The method of claim 1, wherein said secondary nucleotide sequence encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

23. The plant of claim 10, wherein said secondary nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

24. The plant of claim 10, wherein said secondary nucleotide sequence encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

25. The plant of claim 10, wherein said secondary nucleotide sequence is the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

26. The plant cell of claim 18, wherein said secondary nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

27. The plant cell of claim 18, wherein said secondary nucleotide sequence encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

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28. The plant cell of claim 18, wherein said secondary nucleotide sequence is the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

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29. The method of claim 8, wherein said first promoter and said second promoter are the same promoter.

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30. The method of claim 1, wherein said primary nucleotide sequence comprises at least one sequence having at least 80% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.

Sub E1
31. The method of claim 1, wherein said primary nucleotide sequence comprises at least one sequence having at least 90% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.

Sub E1
32. The plant of claim 10, wherein said primary nucleotide sequence comprises at least one sequence having at least 80% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.

Sub E1
33. The plant of claim 10, wherein said primary nucleotide sequence comprises at least one sequence having at least 90% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.